Supplementary Information

Figure S1. Key differences between different RTA-E1 complexes within the asu. The superpositioned Cα traces of two of the six copies of E1 found in the asu representing the different level of interaction between these two E1 subunits with RTA. The E1 subunit with greater interaction with RTA is colored cyan. Residues in this RTA-E1 interface contributing additional hydrogen bonds to the RTA-E1 interface are drawn in stick representation and and color coordinated to their respective main chain color. Hydrogen bonds are drawn as red dashes. The E1 subunit with less interaction with RTA is colored dark gray. The key differences between each RTA-E1 complex within the asu causing the different bsa and H-bonding network comes from deviations at the N-terminus and CDR1 of E1. The N-terminal region is extended by 3 or 4 residues in four of the six E1's within the asu. The additional N-terminal residues interact with RTA residues 156 and 158 burying an additional ~300 Å2 of surface area and contributing as many as four more H-bonds. Four E1's are also missing 1 to 3 residues at the beginning of their CDR1 (residues 26, 27, 28) further reducing the interaction with RTA by as much as ~ 75 Å2 and 3 H-bonds. E1 and V1C7 form salt-bridges with RTA with E1 residue Lys114 interacting with Arg166 of RTA and V1C7 residue Asp59 binding Arg197 in RTA.

Figure S2. V5E1 preferentially associates with ricin over RTA. Sensorgrams from SPR analysis in which ricin-coated chips were probed with V5E1 (blue), V5E1 mixed low (green) or high (orange) RTA concentrations or low (pink) or high (red) ricin concentrations. Relative RU are compared across the treatments.

Figure S3. E1 binds equally to ricin and RTA. Sensorgrams from SPR analysis in which ricin-coated chips were probed with E1 (blue), E1 mixed low (green) or high (orange) RTA concentrations or low (pink) or high (red) ricin concentrations. Relative RU are compared across the treatments.

Supplementary Table 1			
Data Collection			
Complex	RTA-V1C7	RTA-E1	V5E1
APS Beamline	24-ID-C	24-ID-E	24-ID-E
d_{min} (Å)	1.8	3.1	1.7
wavelength (Å)	0.98	0.98	0.98
No. of reflections	2419875	599363	322413
Average redundancy[a]	7.9 (7.6)	6.6(6.5)	3.2 (2.6)
$(I)/(\delta)$[a]	30.7(1.1)	6.4(1.1)	24.6(2.2)
Completeness[a] (%)	99.0 (99.0)	99.8(99.9)	97.6 (93.5)
R_{merge}[a,b] (%)	6.0(99.6)	22.8(140.9)	6.1(37.1)
CC*[c]	(0.95)	(0.92)	(0.92)
Refinement			
Bragg spacings (Å)	49.7-1.85	35.1-3.1	33.6-1.7
Space group	$P3_221$	F222	$P2_1$
Cell parameters: *a, b,c* (Å)	64.8, 64.8, 215.0	239.6, 242.9, 355.7	38.6, 68.1, 71.5 b=92.4
R^d / R_{free}[e] (%)	17.3 / 20.9	22.5 / 27.5	16.4/18.9
No. of unique reflections	49537	93146	43089
No. of waters	231	48	358
Rmsd bond length (Å)	0.018	0.007	0.004
Rmsd bond angle (°)	1.61	1.13	0.816
B-factors (Å^2): main chain/side chain	44.5 / 49.0	86.9 / 90.5	21.6 / 25.3
Ramachandran favored / allowed[f] (%)	97.9 / 100.0	93.0 / 100.0	99.2 / 100.0
PDB code	5J56	5BOZ	5J57

[a] Values in outermost shell are given in parentheses.
[b] $R_{merge} = (\sum | I_i - \langle I_i \rangle |)/\sum | I_i |$, where I_i is the integrated intensity of a given reflection.
[c] CC*=√2CC1/2/1+CC1/2 , where CC1/2 is the correlation coefficient of two split data sets each derived by averaging half of the observations for a given reflection.
[d] $R = \sum | |F_o| - |F_c| | / \sum |F_o|$, where F_o and F_c denote observe and calculated structure factors, respectively.
[e] R_{free} was calculated using 5% of data excluded from refinement.
[f] Calculated using Molprobity.

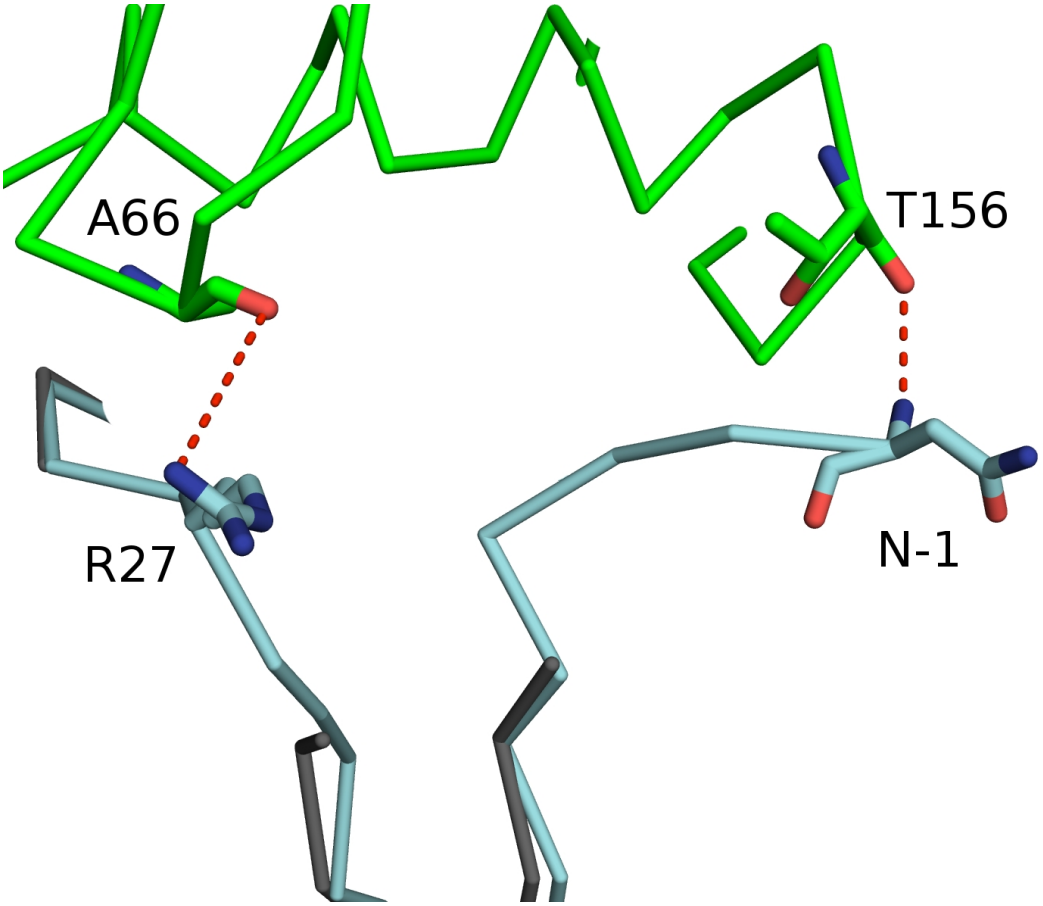
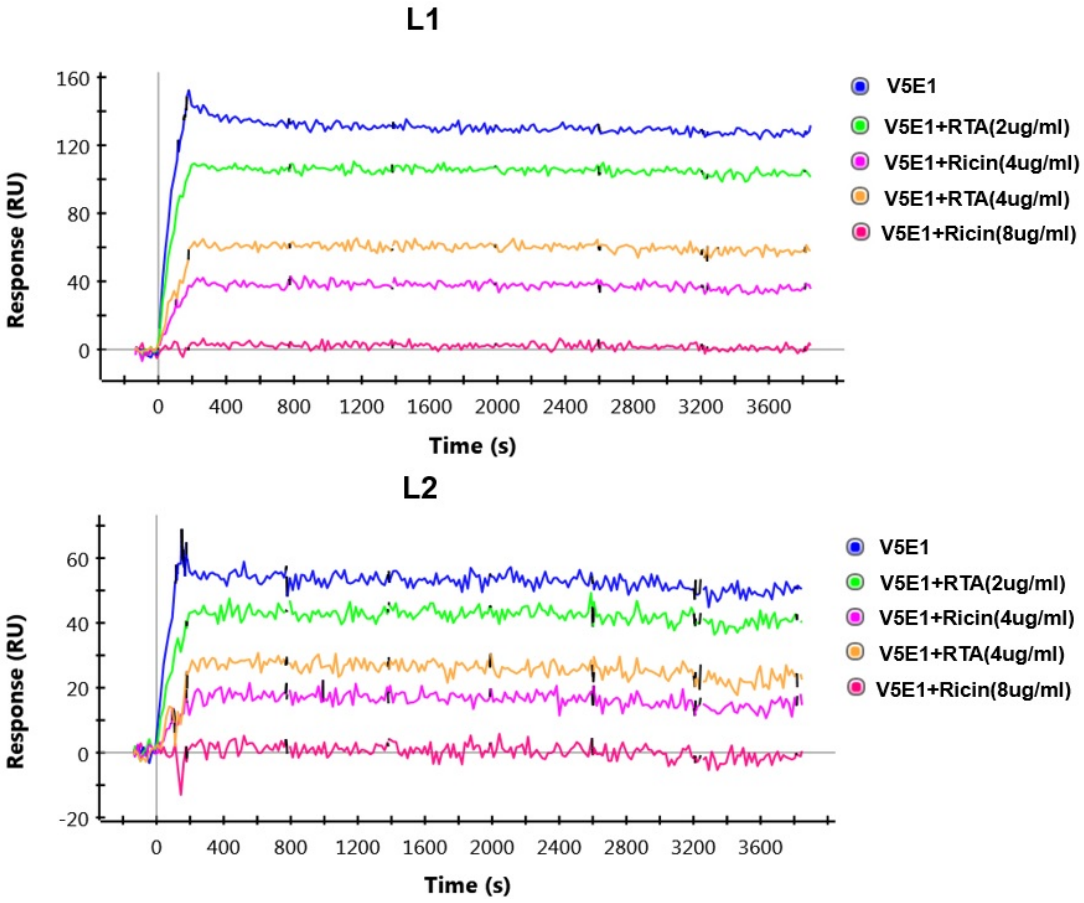


Figure S1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1600
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3200
3600
Time (s)
V5E1
V5E1+RTA(2ug/ml)
V5E1+Ricin(4ug/ml)
V5E1+RTA(4ug/ml)
V5E1+Ricin(8ug/ml)
L2
Response (RU)
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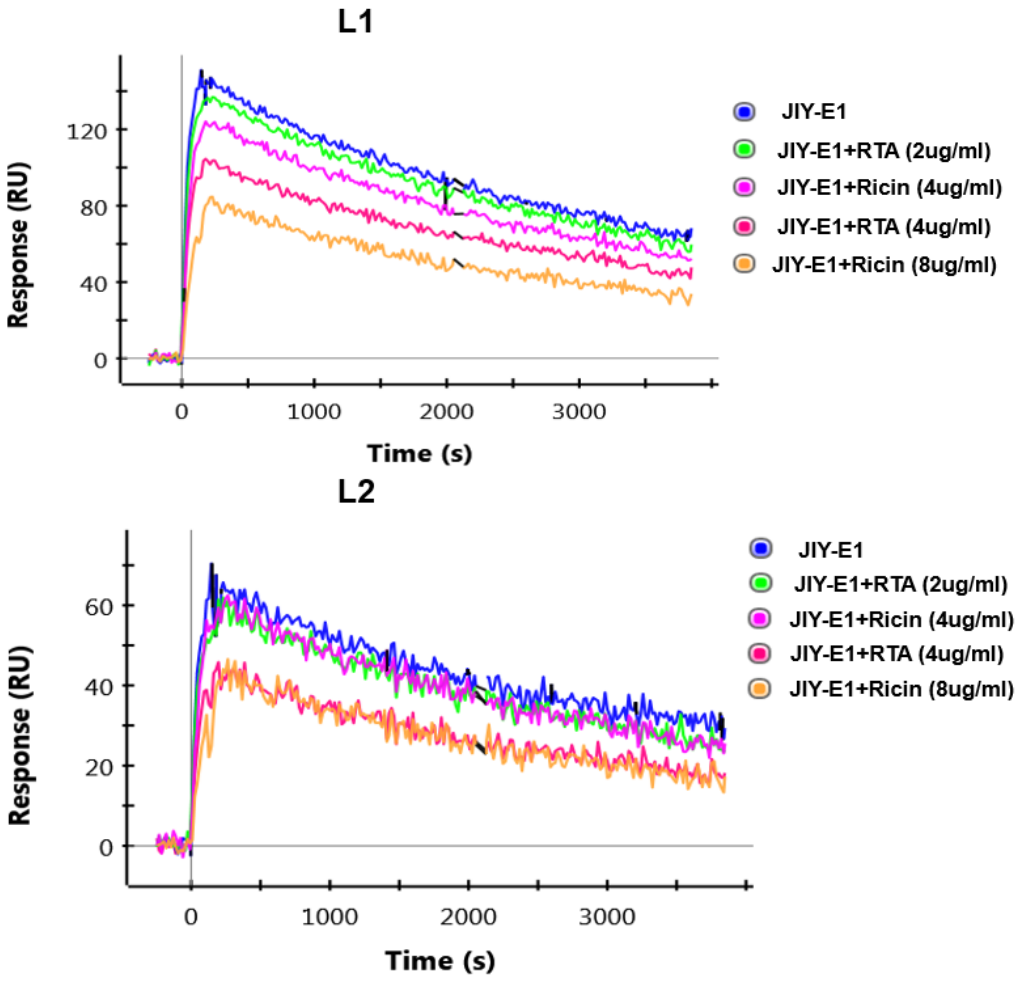
40
20
0
-20
0
400
800
1200
1600
2000
2400
2800
3200
3600
Time (s)
V5E1
V5E1+RTA(2ug/ml)
V5E1+Ricin(4ug/ml)
V5E1+RTA(4ug/ml)
V5E1+Ricin(8ug/ml)

Figure S2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Time (s)
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JIY-E1+RTA (2ug/ml)
JIY-E1+Ricin (4ug/ml)
JIY-E1+RTA (4ug/ml)
JIY-E1+Ricin (8ug/ml)
L2
Response (RU)
60
40
20
0
0
1000
2000
3000
Time (s)
JIY-E1
JIY-E1+RTA (2ug/ml)
JIY-E1+Ricin (4ug/ml)
JIY-E1+RTA (4ug/ml)
JIY-E1+Ricin (8ug/ml)

Figure S3